

17th February 2019

Registration

12:00PM - 2:00PM

Conference Welcome

2:00PM - 2:10PM Auditorium

Chair: Peter Boag

Acknowledgment of Country - Marnie Blewitt

40 Years of Lorne Genome

2:10PM - 2:15PM Auditorium

Chair: David Tremethick

Opening Lecture

2:15PM - 3:00PM Auditorium

Chair: Archa Fox

2:15 PM Joan Steitz

Viral Noncoding RNAs: Diversity in Form and Function abs# 1

Afternoon Tea

3:00PM - 4:00PM Exhibition Hall

Session 1: Julian Wells Medal/Nuclear Organization and Chromosome Structure

4:00PM - 5:30PM Auditorium

Chairs: Andrew Perkins & Anne Voss

4:00 PM Patrick Tam

To be confirmed abs# 26

4:35 PM David Tremethick

Redefining the nucleosomal architecture of active and inactive promoters in the context of cellular plasticity and cancer abs# 4

5:10 PM Mark Pinese

The Medical Genome Reference Bank: Whole genomes and phenotype of 2,570 healthy elderly abs# 101

5:13 PM Tim Hore

Erasing epigenetic memory: Understanding the kinetics and specificity of active DNA demethylation abs# 102

5:16 PM Jane E.A. Reid

Lonely single-stranded DNA seeks RNA ... abs# 103

5:19 PM Dea Slade

PHF3 binds RNA polymerase II via the SPOC domain and regulates transcription of neuronal genes abs# 104

5:22 PM Quentin Gouil

Using long read sequencing to detect imprinted DNA methylation abs# 105

5:25 PM Alyson Ashe

Transgenerational epigenetic inheritance is a complex, multi-step process. abs# 106

Welcome Reception

6:45PM - 8:30PM Lorne Surf Club

Poster Session 1

8:30PM - 10:30PM Exhibition Hall

Jose Alquicira

Cell type prediction at single-cell resolution abs# 107

Joshua Anderson

Characterisation of NHL-2 in small RNA pathways of *Caenorhabditis elegans*. abs# 108

Paul W Angel

The Cell Landscape in Stemformatics abs# 109

Brendan R. E. Ansell

Functional genomics of the retina - insight through transcriptomics abs# 110

Lisa-Marie Appel

The SPOC domain: A novel reader of the CTD code abs# 111

David B Ascher

Using protein structure and function information to predict and understand variant pathogenicity abs# 112

May T Aung-Htut

Late onset Pompe disease: rescue of acid alpha-glucosidase expression by splice modification abs# 113

Francisco Avila Cobos

Assessing the biological signal of different RNA fractions for computational deconvolution of healthy tissues abs# 114

Sureshkumar Balasubramanian

Planting ideas for medicine : Use of Arabidopsis as a model to study genetics of triplet repeat expansions abs# 115

Charles C Bell

Enhancer reprogramming overcomes pervasive non-genetic drug resistance in AML abs# 116

Vinod Benjamin

H3.3S31ph is important for telomeres heterochromatin maintenance in ES cells abs# 117

Taylah Bennett

Glucocorticoid Induced Leucine Zipper is a threshold setter for CD8+ T cell activation and differentiation abs# 118

James Blackburn

Diagnosing Fusion Genes in Cancer Using Targeted RNA Sequencing abs# 119

Daniela P Borges

Investigating the potential use of RNA polymerase 1 transcription inhibitors in the treatment of MDS abs# 120

Parice A Brandies

Koala MHC: Perks of a PacBio Genome abs# 121

Marina R Carpinelli

The Grainyhead-like 2/Zeb1 axis maintains the balance between epithelial and mesenchymal cells during palate closure. abs# 122

Patricia Carreira

Molecular mechanism of L1 retrotransposon activation. abs# 123

Gulrez Chahal

The Intercellular Tight Junction and Spontaneous Coronary Artery Dissection. abs# 124

Wing Fuk Chan

A putative novel enhancer RNA regulates the expression of Gata3 abs# 125

Zac Chatterton

PERIPHERAL MONITORING OF NEURODEGENERATION IN FRONTOTEMPORAL DEMENTIA AND HEALTHY CONTROLS USING CELL-FREE DNA METHYLATION abs# 126

Hyung-Wook Choi

Characterisation of UBF1-like HMG-box proteins in *D. melanogaster*. abs# 127

Jarny Choi

Stemformatics: visualise and download curated stem cell data abs# 128

Scott Cohen

Electron microscopy of the human telomerase enzyme complex
Electron microscopy of the human telomerase enzyme complex abs# 129

Yolanda Colino-Sanguino

Histone acetyltransferase p300 acetylates histone variant H2A.Z preferentially at H4 acetylated nucleosomes. abs# 130

Rhys Colson

The *C. elegans* TRIM protein NHL-2 and its role in the let-7 miRNA pathway abs# 131

Mark A Corbett

Expansion of an ATTTTC short tandem repeat is a frequent cause of familial adult myoclonic epilepsy abs# 132

Peter A Crisp

Accumulation of heterozygous DNA methylation changes generates new epialleles in clonal apple tree lineages abs# 133

Brittany Croft

Human and mouse FGF9 mutations affect male sex determination abs# 134

Mauro D'Amato

Looking for genes where the sun don't shine: the genetics of bowel symptoms and function abs# 135

Glenn D'Cunha

Evaluation of the GATK Best-Practice Workflow for Clinical Whole Genome Sequencing abs# 136

Tasman Daish

Analysis of novel sex biased long non-coding RNA candidates in egg laying mammals. abs# 137

Carolyn de Graaf

Haemopedia RNA-seq: a database of gene expression during haematopoiesis in mice and humans abs# 138

Caroline Delandre

Profiling the chromatin landscape of the *Drosophila* mushroom body abs# 139

Panchamee Ms Dharmadasa

Impact of varying cadmium concentration on gene expression and reproduction in *E. fetida* abs# 141

Thao D Dinh

Context is all - Progesterone receptor-chromatin binding properties and implications on tissue-specific gene expression in mouse reproductive tissues abs# 142

Radoje Drmanac

DNA Nanoballs and Single-Tube LFR: Affordable "Perfect" Genome Sequencing abs# 143

Qian Du

Consequences of Altered DNA Methylation on DNA Replication Timing abs# 144

Tansel Ersavas

Analysis of Single Cell Data Using Deep Learning abs# 145

Eduardo Eyras

Reference-free reconstruction and error correction of transcriptomes from Nanopore long-read sequencing abs# 146

Eduardo Eyras

The functional and immunogenic impacts of RNA-processing alterations in MLL-rearranged infant acute leukemia abs# 147

Natasha Fahey-Lozano

Control of cell competition by cell shape regulators in tissue development and cancer abs# 148

Zheng Fan

CDK12 and 13 regulate RNA Pol II transcription elongation rates abs# 149

Andrew W Farrell

The Role of Planar Cell Polarity in the Initiation of Prostate Cancer abs# 150

Katie A Fennell

Exploring dynamics of non-genomic resistance in AML at the single-cell level abs# 151

James M Ferguson

SquiggleKit: A toolkit for manipulating nanopore signal data abs# 152

Selene L Fernandez-Valverde

Splicing conservation signals in plant long non-coding RNAs abs# 153

Rita Ferreira

RNA polymerase I therapy: the second generation abs# 154

Christoffer Flensburg

Unlocking somatic SNV and CNA calling with RNA-Seq abs# 155

Natalya Frolows

Bioorthogonal RNA labelling in *Caenorhabditis elegans* abs# 156

Emma H Gail

Systematic mapping of molecular interactions within the epigenetic modifier complex PRC2 provides a mechanistic framework for its functional diversity abs# 157

Irene Gallego Romero

Characterising functional genetic variation in Island Southeast Asia abs# 158

Naiara Garcia Bediaga

Multi-level chromosomal reorganization underlying activation of human T cells abs# 159

Michael Geng

Bona fide DNA methylation readers FOXK1/2 participate in cell cycle regulation and are required for vertebrate embryogenesis abs# 160

Amee J George

Genome-wide loss of function screens to determine the molecular mechanism(s) underlying the nucleolar surveillance response abs# 161

Patricia Gerdes

Reprogramming activates retrotransposons in mouse induced pluripotent stem cells abs# 162

Zoe L Grant

Histone acetyltransferase HBO1 regulates endothelial cell gene expression during angiogenesis abs# 163

Jeannette JCH Hallab

Elk1 in Congenital and Late Onset Cardiac Disease: at the Heart of the Matter abs# 164

Zina Hamoudi

A functional genomics approach to identify novel analgesic targets abs# 165

Paul Harrison

Measuring alternative polyadenylation from single cell RNA-seq with precision weights abs# 166

Margaret R Heider

Enzymatic Methyl-Seq: Next Generation Methylomes abs# 167

Thomas N Heider

Improved genome assembly of the tammar wallaby provides a new opportunity to analyze X chromosome evolution in mammals abs# 168

Peter F Hickey

Genome-wide analysis of DNA methylation in samples from the Genotype-Tissue Expression (GTEx) project abs# 169

Tanya Soboleva

Mapping histone variant H2A.B post translational modifications and its interactome in cancer context abs# 170

Joy Kang

QuickExtract- Fast & Easy DNA Extractions For End-point Genotyping PCR Applications abs# 17

Niall P Keegan

Molecular Beacons as a Tool for Visualising Random Autosomal Monoallelic Expression of GHR in Human Lymphoblasts abs# 172

Andrew Keniry

Unlocking female ES cells for research abs# 173

Thang M Khuong

Nerve injury drives a heightened state of vigilance and neuropathic sensitisation in *Drosophila*
abs# 174

Calvin A Kraupner-Taylor

Mispriming of reverse transcription at GAA repeats masks genuine transcript truncations induced
by triplet repeat expansions in eukaryotes abs# 175

Heena V Lad

Dissecting the pleiotropic function of whirlin in the mammalian system. abs# 176

Charlene Lam

New Direct Targets of JAK-STAT signalling which underpin human myeloproliferative neoplasms
(MPNs) abs# 177

Eunice Lee

The role of the piRNA pathway in ovarian and prostate cancer progression abs# 178

Nayla Leon

Loss of ATRX in Sertoli cells leads to DNA double strand breaks at a single PML nuclear body abs#
179

Jasmine Li

H3K27ME3 RESTRAINS CELLULAR SUPPORT PROCESSES REQUIRED FOR T CELL DIFFERENTIATION
abs# 180

Man Tat Lau

Systematic Functional Identification of Cancer Multi-Drug Resistance Genes abs# 181

Iain Searle

Connecting the dots of RNA modifications and small RNA profiles in *arabidopsis thaliana* abs#
182

18th February 2019

Breakfast Workshop: Long Read Sequencing

7:30AM - 8:40AM Horizons Room

Chair: Joseph Powell

Micro Break

8:40AM - 8:50AM Auditorium Foyer

Session 2: Big Data Science

8:50AM - 10:15AM Auditorium

Chairs: Juliet French & Greg Neely

8:50 AM Christopher Mason

A year of human spaceflight: (epi)genome changes, RNA responses, and mtDNA spikes abs# 10

9:25 AM Melanie Bahlo

GWAS, metabolites and Mendelian disorders: identifying the genetic drivers of MacTel, a rare, but complex eye disorder abs# 11

9:50 AM Emily SW Wong

Early origin of developmental enhancers in animals abs# 12

Morning Tea

10:15AM - 11:00AM Exhibition Hall

Session 3: Gene Regulation

11:00AM - 12:42PM Auditorium

Chairs: Ewa Michalak & Austen Ganley

11:00 AM Haruhiko Siomi

De novo DNA methylation punctuated with relaxed 3D chromosome architecture including transposon-rich heterochromatin opening during gonocyte abs# 13

11:35 AM Jason Moffat

To be confirmed abs# 14

12:10 PM Brittany Croft

Human sex reversal is caused by duplication or deletion of core enhancers upstream of SOX9 abs# 15

12:22 PM Andrew Jarratt

Setdb1 regulates JAK-STAT signalling by repressing Suppressor of Cytokine Signalling 3 (Socs3) expression abs# 16

Lunch

12:45PM - 1:15PM Exhibition Hall

Afternoon Workshop: A career = You + Science + Audience

1:15PM - 2:45PM Horizons Room

Chair: Traude Beilharz

Barbara Cheifet

Publishing for Impact abs# 17

Micro Break

2:45PM - 3:00PM Auditorium Foyer

Session 4A: Regulation of Gene Expression

3:00PM - 4:00PM Auditorium

Chairs: Ryan Lister & Megan Bywater

3:00 PM Chen Davidovich

RNA exploits an exposed regulatory site to inhibit the histone methyltransferase PRC2 abs# 18

3:15 PM Megan J Bywater

Rescue of Myc transcriptional activity in the heart unlocks its proliferative capacity abs# 19

3:30 PM Scott Berry

Coordinating genome expression with cell size and shape abs# 20

3:45 PM Simon Junankar

Multi-dimensional analysis of the breast tumour microenvironment at single-cell resolution abs# 21

Session 4B: Disease & Development

3:00PM - 4:00PM Horizons Room

Chairs: Kate Quinlan & Tamas Fischer

3:00 PM Joe Kin Tung Tam

Mapping promoter-enhancer interactions of neuromuscular disease genes abs# 22

3:15 PM Sarah Stephenson

Cellular characterisation of brain malformation using single nuclei RNA-seq. abs# 23

3:30 PM Keryn G Woodman

Using CRISPR gene editing coupled to high-throughput functional assays to improve diagnosis of rare neuromuscular diseases. abs# 24

3:45 PM Tracy M Bryan

Chromosome structure at telomeres: resolution of G-quadruplexes by telomerase abs# 25

Afternoon Tea

4:00PM - 4:30PM Exhibition Hall

Session 5: Noncoding RNA and RNA Regulation

4:30PM - 6:23PM Auditorium

Chairs: Alistair Forrest & Minna-Liisa Anko

4:30 PM Mikiko Siomi

Requirements for multivalent Yb body assembly in piRNA-mediated transposon silencing in *Drosophila* abs# 27

5:05 PM Sue Fletcher

Interaction of modified oligonucleotides with nuclear proteins, formation of novel nuclear structures and sequence-independent effects on RNA processing abs# 28

5:30 PM Maria I Bergamasco

Regulation of neural development genes through histone acetylation abs# 201

5:33 PM Mahdi Zeraati

Visualization and genome-wide mapping of i-Motif DNA structures abs# 202

5:36 PM Michael B Clark

Long-read sequencing reveals the expression and splicing profiles of neuropsychiatric disease genes in human brain abs# 203

5:39 PM Timothy M Johanson

Pax5 organises the B cell genome in three-dimensions independent of transcription abs# 204

5:42 PM Tina Bianco-Miotto

lncRNA expression and function in the human placenta abs# 205

5:45 PM Brendan Russ

Order and disorder in the nucleus - how chromatin folding and misfolding impact T cell differentiation abs# 206

Dinner Break

6:25PM - 8:30PM

Poster Session 2

8:30PM - 10:30PM Exhibition Hall

Krystle Lim

CDK9 function in erythroid enucleation abs# 207

Jamie B Littleboy

Molecular Dissection of Box Jellyfish Venom Cytotoxicity Highlights an Effective Venom Antidote abs# 208

Lipin Loo

Single-cell transcriptomic analysis of mouse neocortical development abs# 209

Lana C Ly

Investigating the role of ZBTB7A homodimerisation in foetal γ -globin repression abs# 210

Charlene M Magtoto

The ZYG11 family - keeping cells in shape abs# 211

Sophia Mah

Histone readers required for heart epicardium formation and differentiation abs# 212

John Manion

SETDB2 mutations suppress pain perception in flies and mice, and cause congenital insensitivity to pain in humans abs# 213

Theo Mantamadiotis

CREB-mediated transcription integrates diverse upstream pathways to modulate oncogenic signals abs# 214

Sarah S Maranhao

Antiproliferative and autophagic effects caused by a new 2-quinoxaliny-hydrazone in colorectal cancer cells abs# 215

Gabriella E Martyn

ELEVATED FOETAL GLOBIN CAUSED BY A NATURAL REGULATORY MUTATION WHICH CREATES A DE NOVO GATA1 SITE abs# 216

Natasha Masand

Identification and functional characterization of evolutionarily conserved cancer testis antigens (CTAs) abs# 217

Elsbeth McLennan

The devil inside: Preliminary dietary analysis reveals a broad depth of prey items in an island population of Tasmanian devils (*Sarcophilus harrisi*) abs# 218

Riley McMahon

A mechanistic insight into building the embryonic head abs# 219

Helen M McRae

The histone reader protein, PHF6, is a new tumour suppressor abs# 220

Rita Mejzini

Investigating Antisense Oligonucleotide Therapeutics for Amyotrophic Lateral Sclerosis abs# 221

Michal Milgrom Hoffman

Mammary stem cell hierarchy maintenance by GPSM2 and asymmetric cell division abs# 222

Zhenhua Ming

NT2/D1 cells model SOX9 function in the mammalian testis abs# 223

Namitha Mohandas

Epigenome-wide association studies (EWAS) of neurodevelopmental disorders using monozygotic twins abs# 224

Luke W Molesworth

ATZ-1 influences meiosis and maintains germline chromosomal stability in *Caenorhabditis elegans* abs# 225

Alison Morey

Remodelling the interior: How the nucleus is reconfigured to regulate CD8+ T cell differentiation. abs# 226

Walter Muskovic

Evolutionary sequence conservation reveals the majority of human long non-coding RNAs are likely non-functional abs# 227

Alina Naveed

NEAT1 long noncoding RNA isoform-switching using antisense oligonucleotides regulates paraspeckle formation in high-risk neuroblastoma cells abs# 228

Lucas M Newton

How did the red blood cell lose its nucleus? abs# 229

Hieu T Nim

Systems Analysis of Adult Tissue Fibroblasts Transcriptomic Identity abs# 230

Aisling O'Connor

Whole genome CRISPR/Cas9 screens identify regulators of the DNA replication stress response
abs# 231

Oscar Ortega-Recalde

Zebrafish preserve germline epigenetic memory globally but demethylate and amplify sex-linked rDNA during feminisation abs# 232

Lisa Oyston

Systematic functional validation of Parkinson's disease GWAS identifies MCMBP as a potential therapeutic target abs# 233

Konstantin Panov

The novel roles of histone demethylase KDM4A abs# 234

Tahlia Perry

First differential transcriptome analysis between juvenile and adult echidna gonads abs# 235

Enrico Petretto

Distinct microglial phenotypes in Alzheimer's disease are controlled by amyloid plaque phagocytosis abs# 236

Bal Hari Poudel

Antisense Oligomer-induced Exon Skipping to Restore Dysferlin Function in LGMD2B Patients abs# 237

Kate GR Quinlan

Eosinophils express secreted factors to directly drive activation of beige adipose tissue abs# 238

Madara Ratnadiwakara

Novel mechanism for stem-cell specific miRNA regulation in development and disease abs# 239

Andre Reis

A synthetic reference unit for measuring quantitative features of genome biology abs# 240

Samuel Ross

Novel DNA demethylation pathway components revealed through reverse genetic screening in vivo abs# 241

Nasim Saadati

Functional analysis of RING and NHL domains of NHL-2 in C.elegans miRNA pathway. abs# 242

Nazmus Salehin

Unveiling the Mixl1 gene regulatory network underpinning mouse endoderm formation using in silico transcription factor binding prediction abs# 243

Werner Scholz

Accelerated Deep learning genomics analysis on GPUs abs# 244

William Schierding

Depletion of Cohesin Factor Rad21 Alters Genome Organisation around Key Transcription Factors During Zygotic Genome Activation abs# 245

Manan Shah

How does a transcription factor find its targets? abs# 246

Raman Sharma

THOC2 variation implicates nuclear mRNA export pathways in neurodevelopmental disorders abs# 247

Nikolay Shirokikh

Translation complex profile sequencing in yeast and human cells abs# 248

Michael Silk

Using the Missense Tolerance Ratio to prioritise disease-causing mutations and to identify novel functional features in gene sequences and protein structures abs# 249

Rebecca Stephens

Scribble on the edge: localisation of a tumour suppressor abs# 250

Julian Stolper

Functional analysis of cardiac-specific regulatory elements involved in heart development and disease abs# 251

Elizabeth S Stout

Phenotypic Heterogeneity in Blood Disorders: The Role of XmnI-G γ in γ -Globin Expression abs# 252

Yu Bo Yang Sun

Using fluorescence polarisation approach to optimise DNA pulldown assay abs# 253

Heidi G Sutherland

Exonic sequencing implicates PRRT2, SLC2A1, SLC4A4 and CSNK1D gene variants in hemiplegic migraine abs# 254

Andrew Szentirmay

Normalase - A Novel Library Normalization Tool for High-Throughput NGS abs# 255

Andres Tapia del Fierro

Smchd1's role in directing long-range chromatin interactions abs# 256

Mark D Temple

The Use of Audio for DNA Sequence Analyses: The Sound of Genes abs# 257

Swapnil Tichkule

Population structure and genetic diversity of *Cryptosporidium hominis* by Whole Genome Sequencing abs# 258

Izabela Todorovski

Genome-wide CRISPR screening reveals loss of STAGA complex activity mediates resistance to CDK7 inhibition abs# 259

Sarah Topfer

Using genome editing to introduce naturally occurring deletional mutations associated with elevated foetal haemoglobin as an approach for treating sickle cell disease and β -Thalassemia abs# 260

Rachael E Turner

Investigating the key mechanisms of alternative polyadenylation abs# 261

Sonika Tyagi

Data-driven approach to screen ncRNA in prokaryotes abs# 262

Michael Uckelmann

USP48 directly antagonises BRCA1-driven histone ubiquitination to regulate chromatin remodelling in response to DNA damage. abs# 263

Thejaani Udumanne

Characterising changes in ribosomal DNA chromatin during malignant transformation abs# 264

Vibha A.V. Udupa

Elucidating the Role of PRC1 Complex in CD8+T Cell Differentiation abs# 265

Lucas van Duin

Predicting individual variation in chromatin architecture from RNA-Seq data abs# 266

Hannah K Vanyai

Hippo pathway effectors, YAP and TAZ, in craniofacial cartilage development abs# 267

Miranda E Vidgen

Developing guidelines for researchers partnering with Aboriginal and/or Torres Strait Islander people and communities to undertake genomic research. abs# 268

Emily J Vohralik

Krüppel-like factor 3 (KLF3) regulates adipose tissue browning via eosinophils abs# 269

Hsiao Voon

The H3.3 K27M Mutation Found in Paediatric Gliomas Alters H3K27me3 at Genomic Repeats abs# 270

Leigh B Waddell

Diagnostic yield from WES, WGS and RNA testing among 213 neuromuscular families: known versus novel disease genes, coding versus non-coding variants. abs# 271

Qianhui Wan

Changes in placental DNA methylation across early human pregnancy abs# 272

C I Wanigasuriya

Smchd1 is a maternal effect gene that plays a significant role in genomic imprinting during early embryonic development abs# 273

Johannes Wichmann

Shining light on the MYST lysine acetyltransferase TIP60 (KAT5) abs# 274

Gigi Wong

Factors beyond binding site complementarity contribute to miRNA-mediated gene silencing abs# 275

Rachel M Woodhouse

Chromatin modifiers SET-25 and SET-32 establish a transgenerational silencing signal in *Caenorhabditis elegans* abs# 276

Feng Yan

Unveil a distinct leukemia stem cell signature using integrative transcriptomics abs# 277

Lu Yang

Identification of a novel partner of KLF3 that plays an important role in KLF3 genome localisation abs# 278

Yuqing Yang

Histone acetyltransferase HBO1 (KAT7) regulates haematopoietic stem cell quiescence, self-renewal and lineage differentiation abs# 279

Olga Zaytseva

Surprising roles for the ssDNA binding protein Psi in *Drosophila* neural stem cells: more than MYC transcription? abs# 280

Song Zhang

Roles of RNA and DNA binding capacity of NONO in neuroblastoma abs# 281

19th February 2019

Session 6: Disease and Disease Genomics

9:00AM - 10:25AM Auditorium

Chairs: Leonie Quinn & Patrick Humbert

9:00 AM Nathan Palpant

Comparative analysis of H3K27me3 domains establishes a repressive index for inferring regulatory genes governing cell identity from any chordate cell type abs# 35

9:25 AM David Thomas

MTOR signaling orchestrates stress-induced mutagenesis facilitating adaptive evolution in human cancers abs# 36

9:50 AM Andrew Jackson

Disordered epigenetic regulation and human growth abs# 37

Morning Tea

10:25AM - 11:00AM Exhibition Hall

Session 7: Evolution and Population Genetics

11:00AM - 12:20PM Auditorium

Chairs: John Bowman & Irene Gallego Romero

11:00 AM Jonathan Jones

Exploiting and dissecting plant immune receptor diversity abs# 38

11:35 AM Katherine Belov

Using genomics to conserve Australia's biodiversity abs# 39

12:00 PM Murray P Cox

Multiple deeply divergent Denisovan ancestries in Papuans abs# 40

Student Lunch

12:20PM - 1:15PM Lorne Central

Lunch

12:20PM - 1:15PM Exhibition Hall

Lorne Genome AGM

1:15PM - 2:30PM Horizons Room

Session 8A: Computational Biology

2:30PM - 3:30PM Auditorium

Chairs: Eduardo Eyraes & Sonika Tyagi

2:30 PM Ozren Bogdanovic

FOXK proteins are evolutionarily conserved DNA methylation readers required for vertebrate embryogenesis abs# 41

2:45 PM Mahdi Moradi Marjaneh

Non-coding RNAs underlie genetic predisposition to breast cancer abs# 42

3:00 PM Mirana Ramialison

cis-regulation of heart development and disease abs# 43

3:15 PM Amanda Khoury

'Constitutively bound CTCF sites regulate higher order 3D chromatin architecture abs# 44

Session 8B: Epigenetics/genomics

2:30PM - 3:30PM Horizons Room

Chairs: Owen Marshall & Marnie Blewitt

2:30 PM Anja S Knaupp

Transient and Permanent Reconfiguration of Chromatin and Transcription Factor Occupancy Drive Reprogramming abs# 45

2:45 PM Omer Gilan

Domain-selective BET inhibitors uncover divergent functions for the tandem bromodomains. abs# 46

3:00 PM Ksenia Skvortsova

Zebrafish as a Lamarckian giraffe: inheritance of the paternal epigenome. abs# 47

3:15 PM Sriharsa Pradhan

UniNicE-seq: accessible chromatin landscape of cells and tissues abs# 48

Afternoon Tea

3:30PM - 3:50PM Auditorium Foyer

Session 9: Chromatin and Epigenetics/Epigenomics

3:50PM - 5:20PM Auditorium

Chairs: Lee Wong & Rhys Allan

3:50 PM Caroline Dean

Epigenetic switching and antisense transcription abs# 50

4:25 PM Susan J Clark

DNA hypermethylation encroachment at CpG island borders in cancer is predisposed by H3K4 monomethylation patterns abs# 51

4:45 PM James Turner

Using marsupials to understand sex chromosome evolution and early embryonic development abs# 52

Micro Break

5:20PM - 5:30PM Auditorium Foyer

Closing Lecture

5:30PM - 6:15PM Auditorium

Chair: Scott Cohen

5:30 PM Steve Brown

The International Mouse Phenotyping Consortium (IMPC): A comprehensive catalogue of gene function for the mammalian genome. abs# 53

Conference Awards & Close

6:15PM - 6:45PM Auditorium

Chairs: Peter Boag & Scott Cohen

Festival of Food

7:30PM - 9:00PM Umisango, Jashn & Lorne Central

Dessert, Dancing & Drinks

9:00PM - 11:59PM Lorne Central

20th February 2019

Buses Depart

9:00AM - 9:05AM

Buses Depart

12:00PM - 12:05PM